

Figure 1

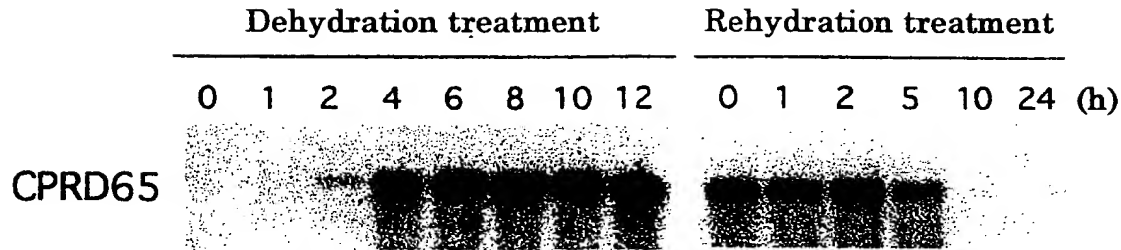
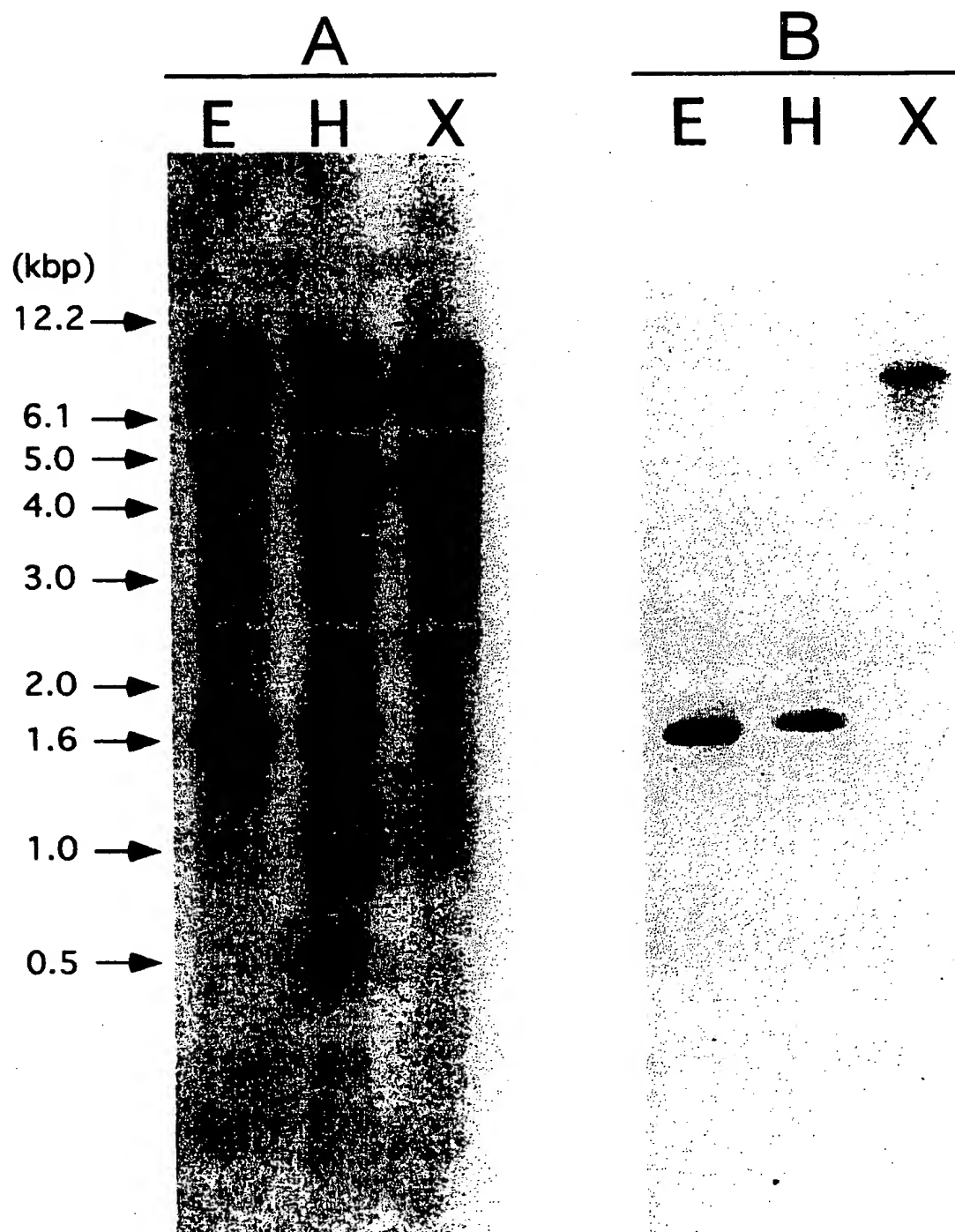


Figure 2

| | | |
|---------|---|-----|
| CPRD65 | PSSASNTWFMATLPSPPFKDLPSTSSPTNLLPLRKTSSTNTITCSLPLHFPKQYQPTSTSTSTATTITPTIKTITITITITPTRETNP | 90 |
| VP14 | MDGLAPPTSVSIIHRHLPA-RSRARASNSVRFSR-RAVSSVPPAEC-LDA-PFHK----PVADLPAPSRKPAAI--AVPGHAAAPKAEG | 79 |
| LeNCED1 | MTTTSF---ATNTWIKT-KLSMPSKEFGFAS-NSISLLKQHN-RSLNINS---SLQAPPILHFPKQSSNYQTPKNNTISHPKQEN- | 80 |
| CPRD65 | LSDTNQLPQKNFLQKAAATALDLVETALVSHRKSLPTADPNQIINGFAPVPEHAADQGLPVIGLIPKCIDGVYRNGANPLYEP | 180 |
| VP14 | -GKKQLNLFQR-AAAAALDAFEEGFANVL---ERPHLESTADPNQIINGFAPVGERPPVHELVEGRIPPFIDGVYRNGANPCFDP | 164 |
| LeNCED1 | -NNSSSSTSKNHLVQKAAAMALDAVESALTKEGSLPTADPNQIINGFAPVPEHPVCSLPVIGLIPKCVQGVYRNGANPLYEP | 169 |
| CPRD65 | VAGHIFDGDGVHAKFTNGALSYACRFETETRLDEKSLGRPVFPKATGELHGHSGIARLLFYARGLFGLVDKSGGVANAGLVY | 269 |
| VP14 | VAGHIFDGDGVHALLRIRNGAESYACRFETETRLDERAIGRPVFPKATGELHGHSGIARLLFYARNACGLVDPSNGGVANAGLVY | 254 |
| LeNCED1 | TAGHIFDGDGVHAKFTNGALSYACRFETETRLDEKSLGRPVFPKATGELHGHSGIARLLFYARGLFGLVDKSGGVANAGLVY | 258 |
| CPRD65 | FNHLLAMSEDDLPYHVRITPNDLITGRDFEQLNSTIAHPKLDPVGGLALSVDVIRPYLYKYPFSPOGKSDVEIPLKEPT | 359 |
| VP14 | FNHLLAMSEDDLPYHVRVADGDLITGRDFEQLNSTIAHPKLDPATGGLALSVDVIRPYLYKYPFSPOGKSDVEIPLKEPT | 344 |
| LeNCED1 | FNHLLAMSEDDLPYHVKVTPTGDLITGRDFEQLNSTIAHPKLDPVSGGLALSVDVIRPYLYKYPFSKNGKSDVEIPLKEPT | 348 |
| CPRD65 | MDFAITENFVYVPOQVVFKLTEMLTGGSPVYDKNKSRFGDLKADANAMRDAPOCFCEHLNNAWEPEETELVVGSCMTP | 449 |
| VP14 | MDFAITENFVYVPOQVVFKLQEMLRGGSPVYDKNKSRFGDLKADANAMRDAPOCFCEHLNNAWEDEATTELVVGSCMTP | 434 |
| LeNCED1 | MDFAITENFVYVPOQVVPKASEMIRGGSPVYDKNKSRFGDLKADANSSOLNWEVPOCFCEHLNNAWEAETTELVVGSCMTP | 438 |
| CPRD65 | ADSIENEEELSVLEIRLNLRTGSTRPIISDAEQ-VILENGVNRNKLGRKTQFAYLAEPPWKGSGFAKVDLSGEVKQMYG | 538 |
| VP14 | ADSIENESDEELSVLEIRLDARTGRSTRAVLPSSQ-ENLENGVNRNKLGRSRYAYLAEPPWKGSGFAKEDLTGELTKFEYG | 523 |
| LeNCED1 | ADSIENEEELSVLEIRLNLRTGSTRKSIENPDEQVNLNGVNRNKLGRKTEYAYLAEPPWKGSGFAKVDLTGEVEKFIYG | 528 |
| CPRD65 | EEKFGGERFLP-----NGQKEDDGYLNFVHDEKWKSELQVNAQNLKLEASIKLPSRVPFGHGTFTISKDRIQA | 612 |
| VP14 | EGRFGGERFLPMDPAAAHPRGDDGYLNFVHDERAGTSELVYNAADIRLEAFVQLPSRVPFGHGTFTIGQLEADA | 604 |
| LeNCED1 | DNKYGGERFLPDP-----NSKEDDGYLNFVHDEKWKSELQVNASLKEAFVQLPSRVPFGHGTFTINANDLADA | 605 |

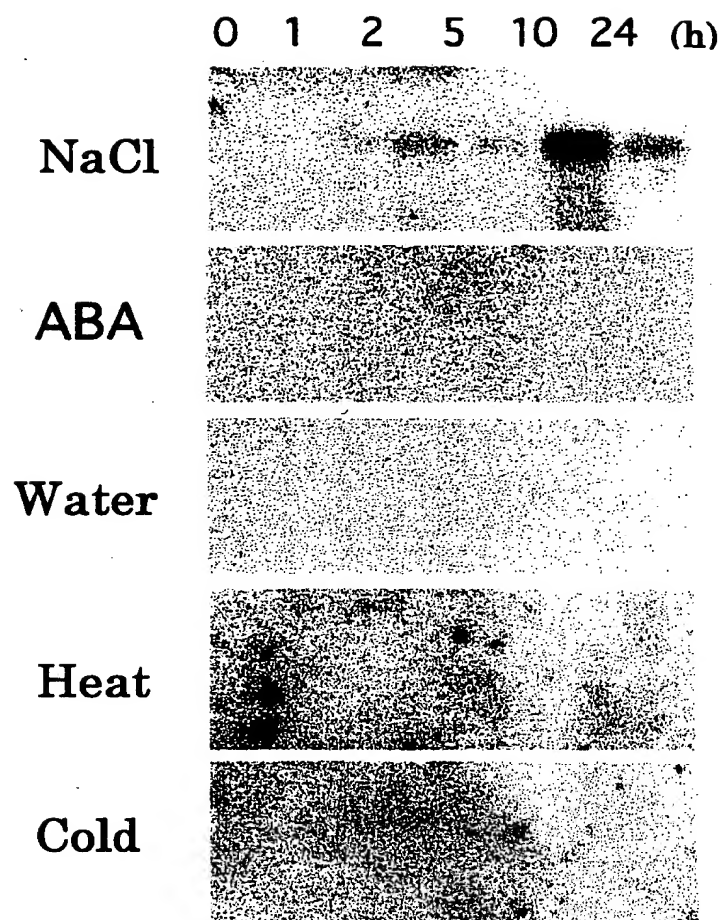
Figure 3



3/15

Figure 4

(A)



(B)

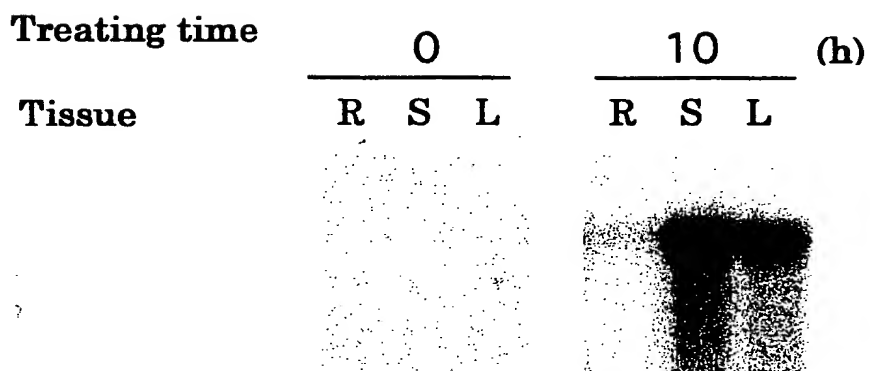
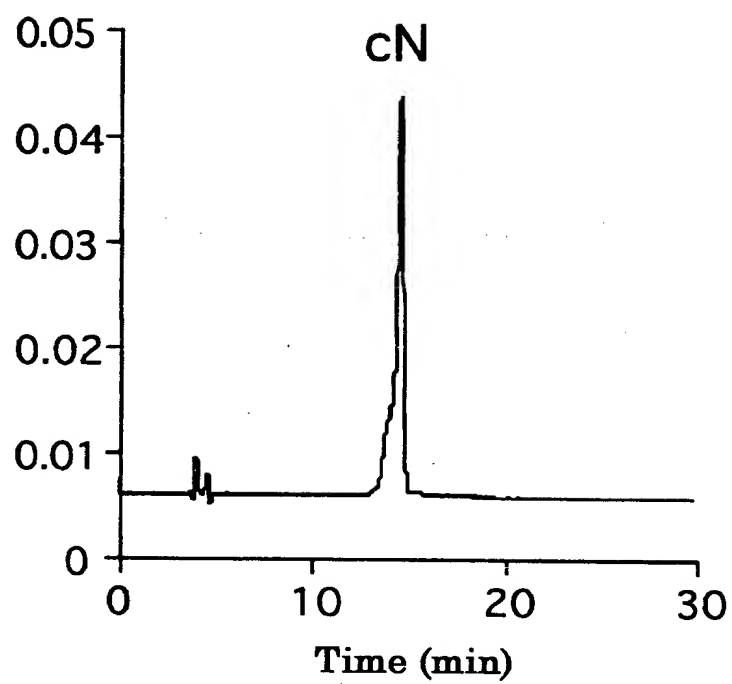


Figure 5

(A)



(B)

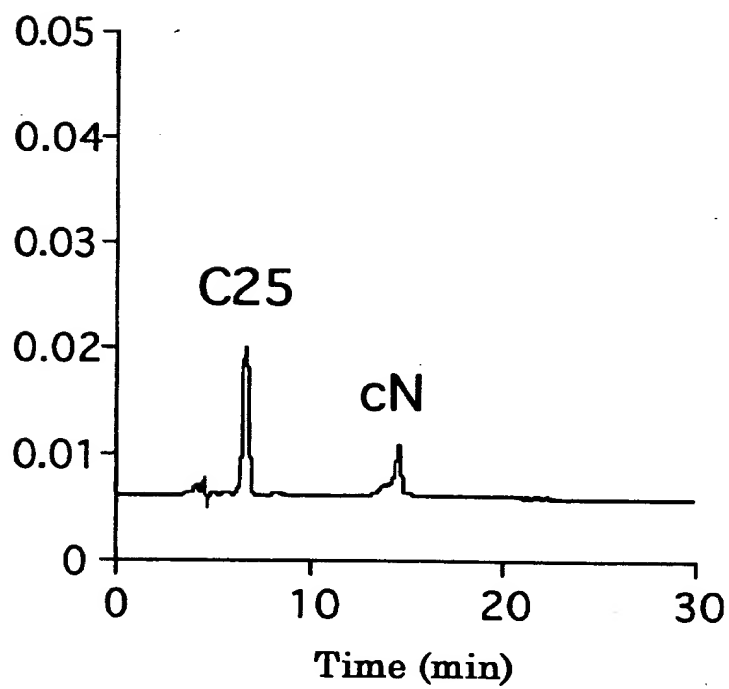
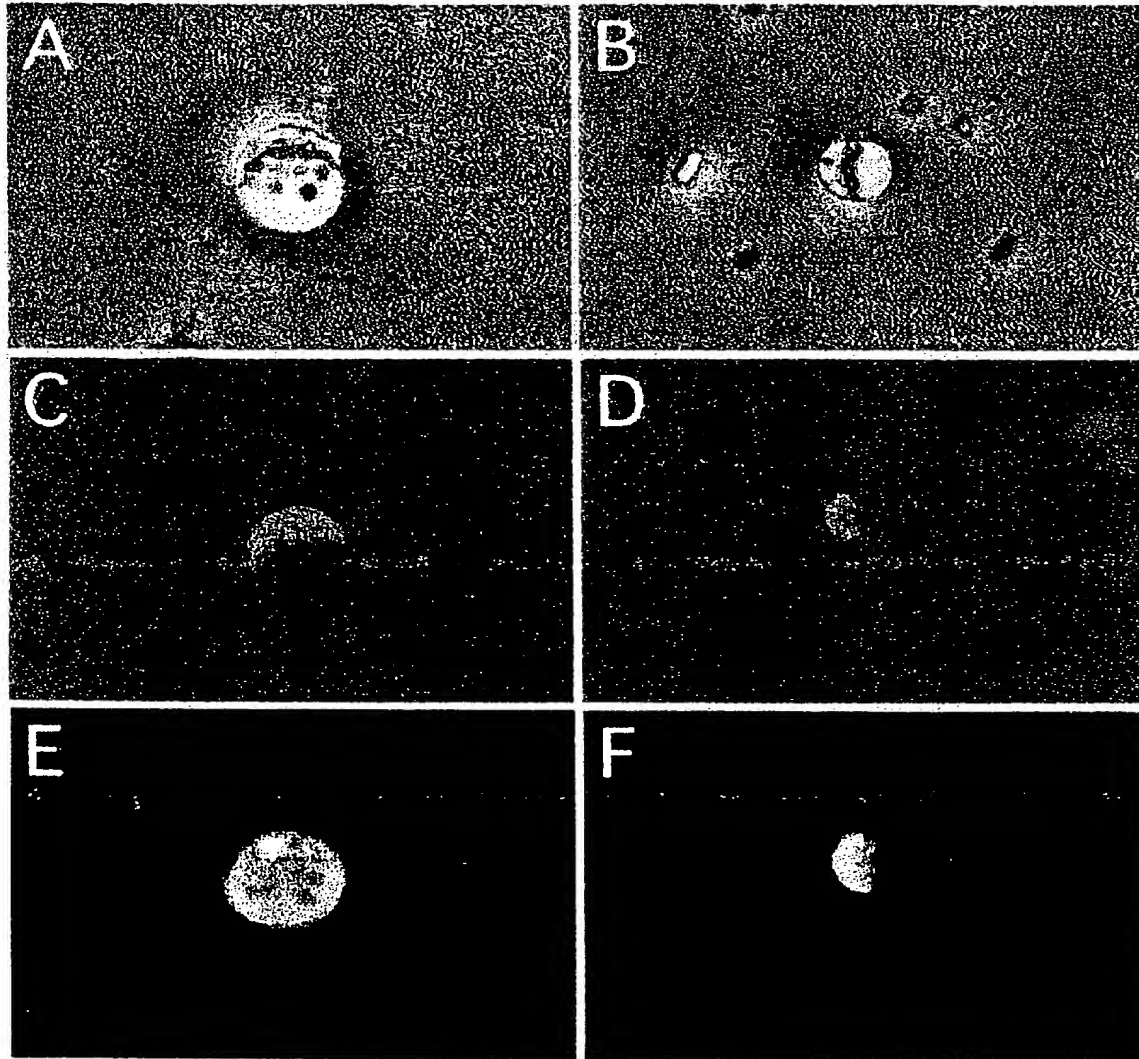


Figure 6



00750000 044004
00000000 00000000

Figure 7

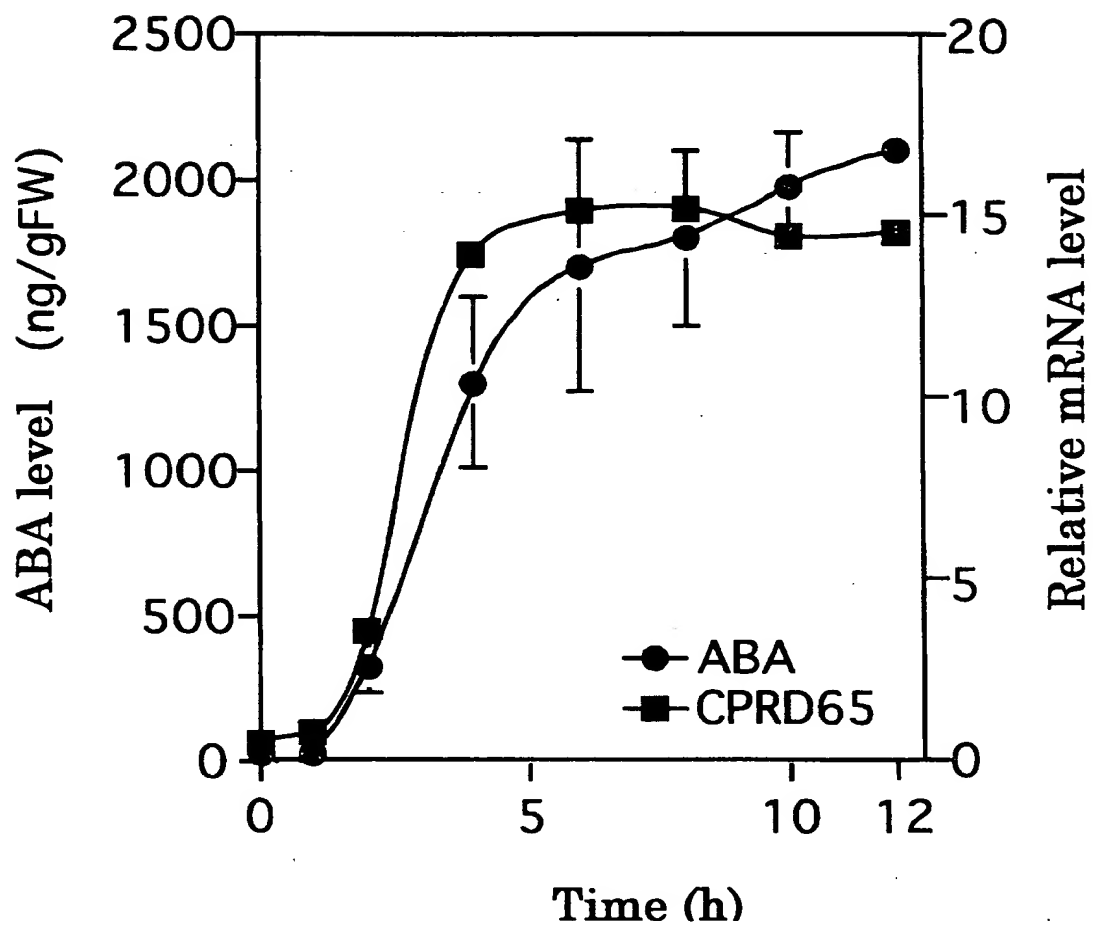


Figure 8

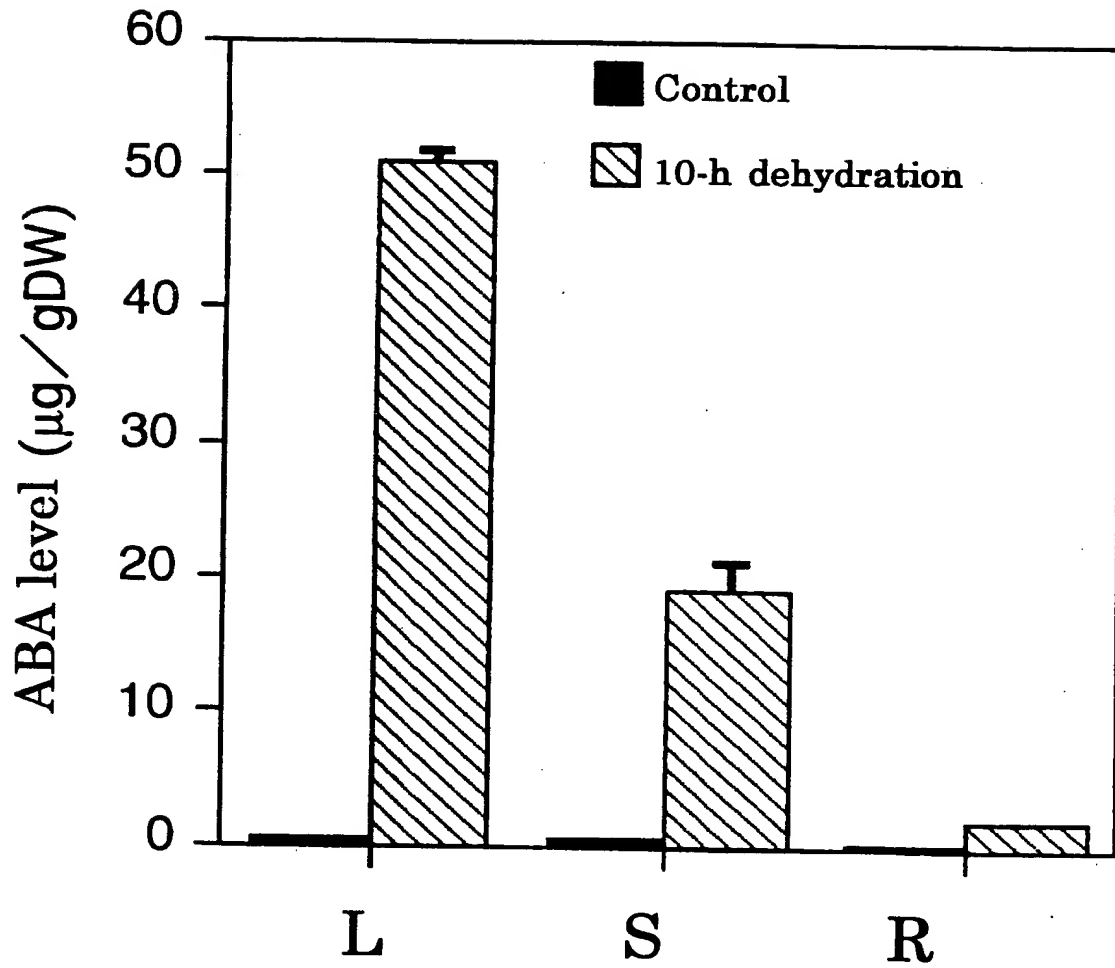


Figure 9

| | | |
|---------|---|-----|
| AtNCED3 | MAS-----FIATAAVSG-RWLGGNHTQP---PLSSSSDLSYCS--SL--PMASRVTRKLNVSALHTPPALH | 61 |
| CPRD65 | MPSSASNTWENATLPSPPFKDL PSTSSPTNLLPLRKTSSNTITCSLQTLHFPKQYQFTSTSTATTITPTPIK | 75 |
| AtNCED3 | FPKQSSNSPIIVKPI--KAKESNTKQNNLFOHAAAHALDAEGLVSHEKLNHPLPKTADPVOIAGNFAPVNEQP | 134 |
| CPRD65 | TTTITTTTPPRETNPLSOTNQPLPQKNFLQKAAALALDVELVYSHERKHPLPKTADPVOIAGNFAPVREHA | 150 |
| AtNCED3 | VRRNLPVVGKIPDSINGVYVRNGANPL EPVGHFFDGDGMVHAVKFEHGHASYACRFTTTRFVQERQLGRPV | 209 |
| CPRD65 | ADQGLPVVGKIPKCIDGVYVRNGANPL EPVGHFFDGDGMVHAVKFTNGHASYACRFTETORL SQEKS LGRPV | 225 |
| AtNCED3 | FPKATGELHGHIGIARLLFYARAAAGIVDPAHGVANAGLVYFNGHLLAMSEDDLPHYVITPNGDLITVGRF | 284 |
| CPRD65 | FPKATGELHGHIGIARLLFYARGLFGIVDGSOGGVANAGLVYFNGHLLAMSEDDLPHYVITPNGDLITVGRY | 300 |
| AtNCED3 | DFDQGLSTMTAHPKIDPESGELFALSVDVSKPYLKYFRFSPDGLKSPDVEILDQPTMHDFAITENFVVVPD | 359 |
| CPRD65 | DFDQGLSTMTAHPKIDPVQGLFALSVDVCKPYLKYFRFSPDGLKSPDVEILKEPTMHDFAITENFVVVPD | 375 |
| AtNCED3 | QQVFKLHEMIGGSPVYDKNKVARFGILKYABSSNIKWIDAPDCFCFHLWNAWEEPETDEVVIGSCMTPP | 434 |
| CPRD65 | QQVFKLHEMIGGSPVYDKNKTSRFGILKYANDANAMRWIDAPDCFCFHLWNAWEEPETDEVVIGSCMTPA | 450 |
| AtNCED3 | DSIFNESENLSVLSSEIRLNLKTGSTRRPIISNEQVNL EAGVNRNMLGRKTFAYLALAEPPVKVSGFAK | 509 |
| CPRD65 | DSIFNESENLSVLSSEIRLNLKTGSTRRPIISDAEQVNL EAGVNRNMLGRKTFAYLALAEPPVKVSGFAK | 524 |
| AtNCED3 | VDLTIGEVKKHLYGDNRYGGEPLFLPGEGGEDEGYILFVHDEKMKSELQIVNAVSLVEATVKLPSRVYPYGF | 584 |
| CPRD65 | VDLTIGEVKKHMYGEEKFGGEPLFLPNGQKEDDGYILFVHDEKMKSELQIVNAQLKLEASTVKLPSRVYPYGF | 598 |
| AtNCED3 | HGTFIGADDLAKQVV | 599 |
| CPRD65 | HGTFIHSKDLRKQA- | 612 |

Figure 10

| | | |
|--------|---|-----|
| AtNCD1 | MSL-LTMMFSGGGIKTMO--AQ-IDLGF-RPIKROPKV-----IKCTVQIDVTELTKGRQLFTRTTAT | 60 |
| AtNCD2 | MSVSSSSSFLS-----STFSLHSS-----LLRRSSSPTLLRNSAVW-----EERSPTINPSNDNRNPKTLHRT | 64 |
| AtNCD3 | MSFTATAAVSGRMLGQNTQPLSSSSQSSLSYCSSLPASRVTRKLNSSALHTPPALHFPKSSNSPATVVK | 75 |
| AtNCD4 | MA-----BKLSDGS-----IIISVHPPS----- | 19 |
| AtNCD5 | MCHSLRSOLLPTKTSRSHLLPQKWNANISRRLLNPKIPTLPDLTSVPVSPVKLPKTPYPNLNLQKLAATMLD | 75 |
| AtNCD1 | P--POHPLRLNIFOKAAATAIDAAERALTSHEQDSPLPKTADPRVOTAGNYSVPVSSVRRNL-TVEGTFDCI | 132 |
| AtNCD2 | NHTLVSSPPKLRPEMLTALFTTVEQVINTFIDPPSRP-SVDPKHLSDNFAPVLDLPPTDCETIHGILPSL | 138 |
| AtNCD3 | PKAKESNTKQNLFORAAAAALDAEGLYSHEKLHELPKTADPSVQIAGNFAPVNEQVRRNL-PWGLKLPDSI | 149 |
| AtNCD4 | -----KGF-----SSKLLDLLERLVKLMHDSLPLHY-----LSGNFAPIRDETTPVKDLVHGFUEPCL | 75 |
| AtNCD5 | KTESIVIPMEQNRPLPKPTPAVQLSGNFAPVNEQVQNG-----LEWGLDIESCL | 127 |
| AtNCD1 | KGYYIRGQNFPEPTAGHFDGQGMHVKIT-NGSASYACRFITRERLVOERLGRPVFPKAIIGELHGS-G | 205 |
| AtNCD2 | NGYYIRGQNFPEPTAGHFDGQGMHVKIT-NGKATLCSRVKITYKMEKOTGAPMFMVSGFGHTAS | 212 |
| AtNCD3 | KGYYIRGQNFPEPTAGHFDGQGMHVKIT-NGSASYACRFITRERLVOERLGRPVFPKAIIGELHGT-G | 222 |
| AtNCD4 | NGEYIRGQNFPEPTAGHFDGQGMHVKIT-NGKATYSRVITSRKOEFFGAQFMK-IGDLKGF-G | 147 |
| AtNCD5 | KGYYIRGQNFPEPTAGHFDGQGMHVKIT-NGSASYACRFITRERLVOERLGRPVFPKAIIGELHGS-G | 201 |
| AtNCD1 | IARLMFYARGLCGLTNONGAGANAGVYFNRLAISEDLPYDKCTOTGLQTVGRYDFDGLKSAHIAH | 280 |
| AtNCD2 | VARGALTAARVLTCQYNPVNGGIANESLAFFSNRFAIGEDLPYVRLTESGLDITGRYDFDGLKSAHIAH | 287 |
| AtNCD3 | IARLMFYARAAAGVDPAGGAGANAGVYFNRLAISEDLPYDKCTOTGLQTVGRYDFDGLKSAHIAH | 297 |
| AtNCD4 | LLMNTGQRLTKLCLDNTYNGGIANALVYHGLALCEDEPYDKVLEGLQTVGRYDFDGLKSAHIAH | 222 |
| AtNCD5 | LARLAEFTARAGIGLVDTGAGANAGVYFNRLAISEDLPYDKCTOTGLQTVGRYDFDGLKSAHIAH | 276 |
| AtNCD1 | PKLQVTKELHALSYVWKKPMLYFRFSPDGKSPLETLPLETITMIDFAITENFWWIPDQWFKLGEM-- | 352 |
| AtNCD2 | PKQDITGETFAFRYPV-FPFLTYFRFDSAGKQKQRMFLPSMTSPFLHDFAITGRHAFETQLGRRMMLDL | 361 |
| AtNCD3 | PKQDPESGELFALSYDVSKMLYFRFSPDGKSPVET-QLDQITMIDFAITENFWWIPDQWFKLPEM-- | 369 |
| AtNCD4 | PKQDPVTGEMFTFGYS-HITFPLIYVTSKQGMHDPVPL-TLSBFLMIDFAITETATMOLPMFRPKEM-- | 293 |
| AtNCD5 | PKQDATTGDLHTLSYMLKPELRYLKFTGCKKTRDVELTLPETITMIDFAITENFWWIPDQWFKLGEM-- | 348 |
| AtNCD1 | ISGKSPV-VFDGKVSRLGMPKDATEASQITWNSPETFCFLNNANESPETEE---IV---VIGSOMSPADSI | 420 |
| AtNCD2 | VLEGGSPVGTQNKITRLG/TPKYAGDESEWFEVPGFNTHATNWDGDS---W---LIAPNIMSTHT | 430 |
| AtNCD3 | IRGGSPV-VYDKQVAFGELDKYAESNDMDAPDCFCFLNNANESPETDE---W---VIGSOMTPDST | 437 |
| AtNCD4 | VKEKMIYSFDPITKARGLPRYAKDELMDPFLPNCFTFNANWEEDE---WLITCRLENPOLDWMSGK | 365 |
| AtNCD5 | IRGGSPV-IYKELKARGLSKQDLTGSDINWMDPDCFCFLNNANESPETEEGDPVIV---VIGSOMSPDST | 419 |
| AtNCD1 | FNEDESLSRVLSEIRNLRTKTRPSLLV--NEDVNLETGW-NRNLGRKTRFAFLATAYPWKVSQFAKVD | 492 |
| AtNCD2 | L-EMDLVHALVEVKIELVITIVRRPTISA-----RNLDFAVI-NPAFLGRCSRYVYALGDMFKLSGVAKLD | 498 |
| AtNCD3 | FNEDENLKSVLSEIRNLNLTGSTRPTISNEQVNLKAGW-NRNLGRKTRFAFLATAYPWKVSQFAKVD | 511 |
| AtNCD4 | VKELENFQNELYEMRPMKTSASQKLSASAVDFPRINECYTGKORYVYGTILDSTAKVTGLKFDLHAEAE | 440 |
| AtNCD5 | FSEGEPTRVLSEIRNLNMTKESNRKIVT----GVNLEAGHI-NRSYVGRKSQVYIALADPWKLSQFAKVD | 489 |
| AtNCD1 | LCTGEMKKYIYGGEYK-G-EPFFLPQN--SGNGEEDGYIFGVHDEETKISELOTINAVNLKLE--ATIK | 560 |
| AtNCD2 | VSKGRODCTVARRMYSGCYGGEFFVARDPGNPEAEEDGYVTVHDEVTGSKFLMDAKSPELETVAVR | 573 |
| AtNCD3 | LTTGEVKKHLYGNRYK-G-EPLFLPGE--GGEDE-----GYLCPVHDEETKISELOTINAVNLKLE--ATIK | 575 |
| AtNCD4 | TGKRLVGGNLIKGYLKG-EGRYGEATVVPREAEEDGYLIFVHDEETKISELOTINAVNLKLE--ATIK | 513 |
| AtNCD5 | IQNGTVSEFNYPSPRG-G-EPCVPPEG--EGEEDK-----GYMGRVHDEETKISELOTINAVNLKLE--ATIK | 553 |
| AtNCD1 | LPFRVPYGFHTIFVDSNELVDL-- | 583 |
| AtNCD2 | LPFRVPYGFHTIFVDSNELVDL-- | 595 |
| AtNCD3 | LPFRVPYGFHTIFVDSNELVDL-- | 599 |
| AtNCD4 | LPFRVPYGFHTIFVDSNELVDL-- | 538 |
| AtNCD5 | LPFRVPYGFHTIFVDSNELVDL-- | 577 |

Figure 11

10/15

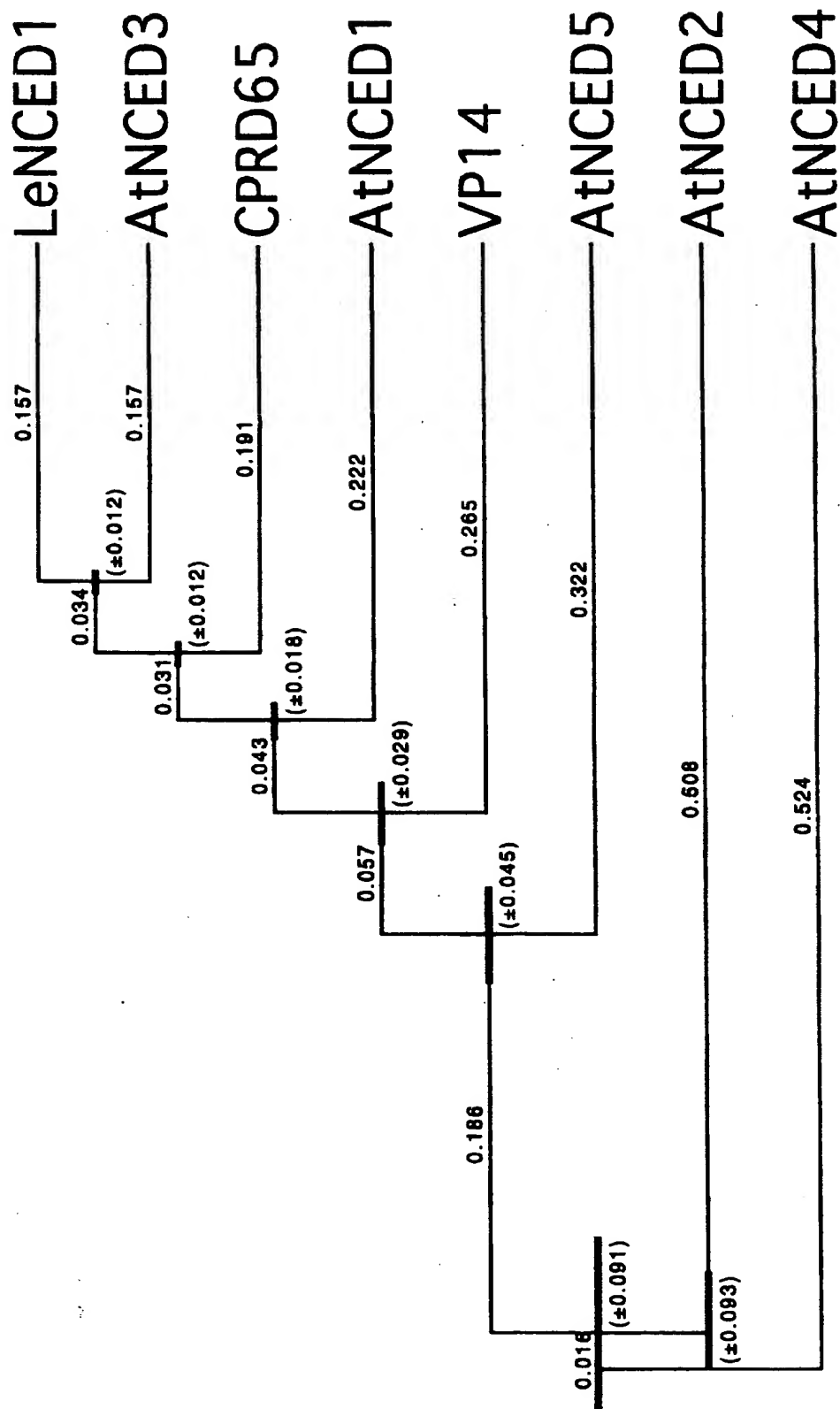


Figure 12

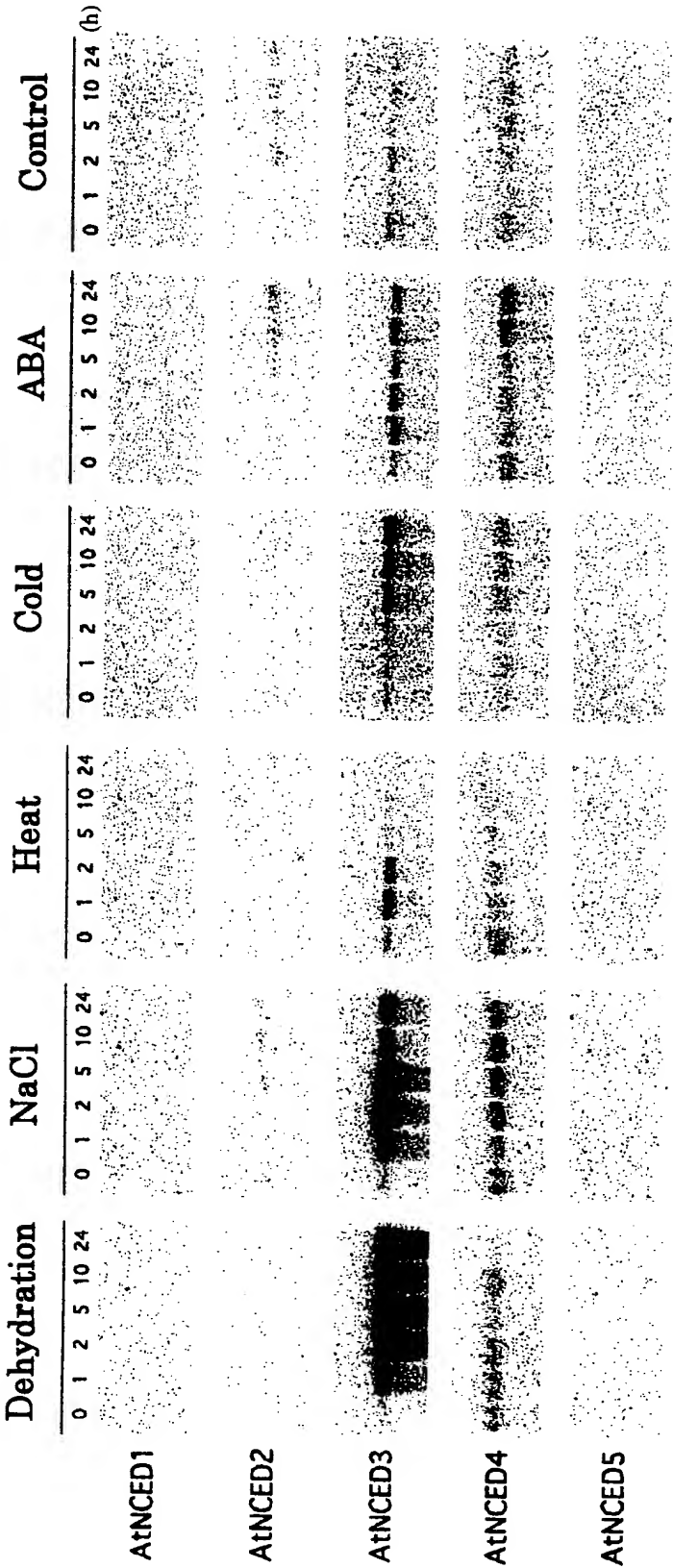


Figure 13

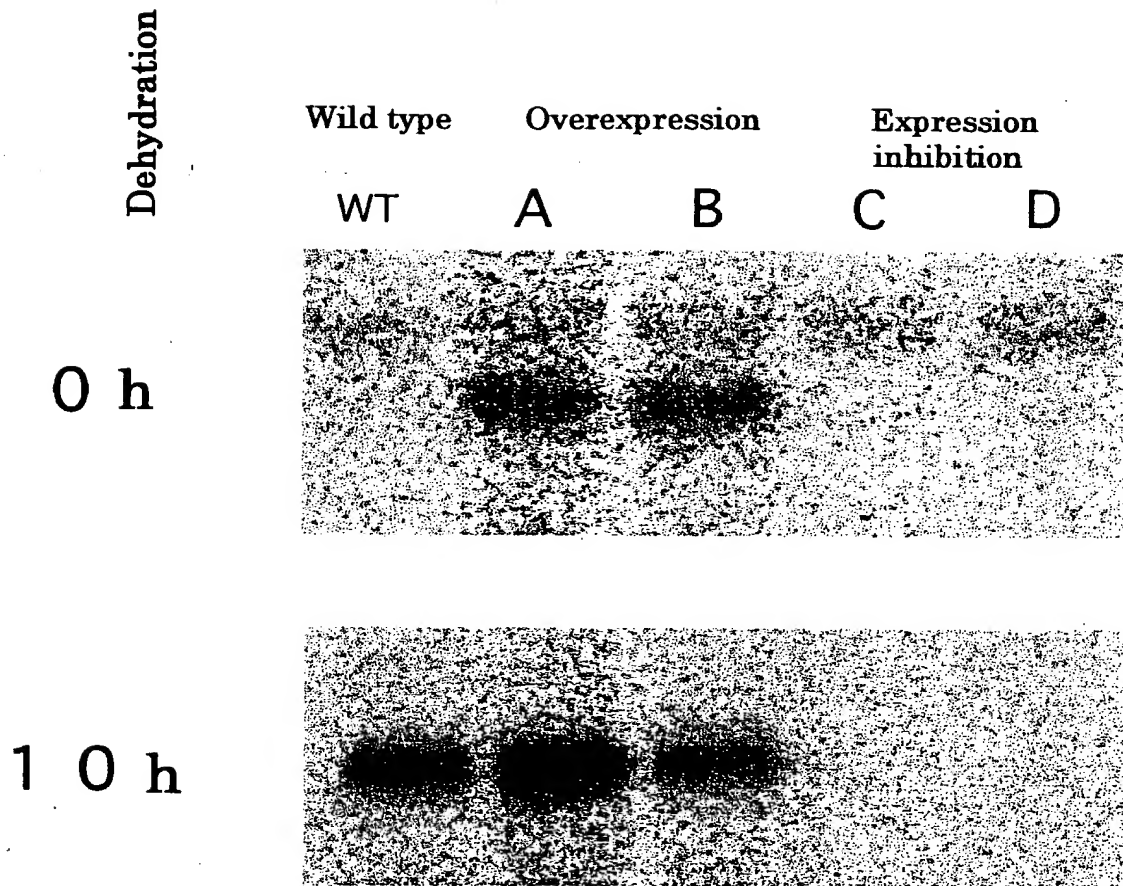


Figure 14

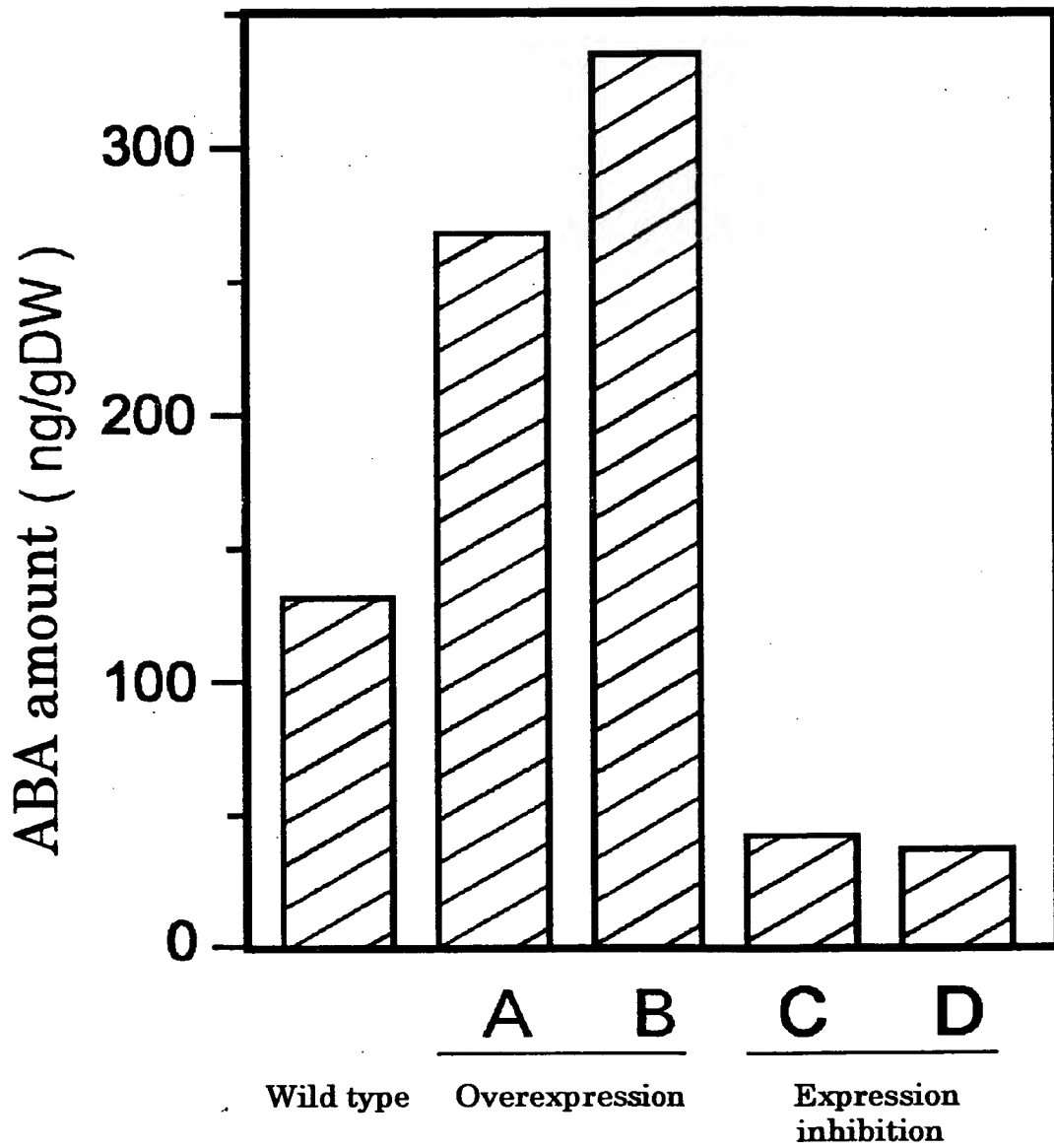
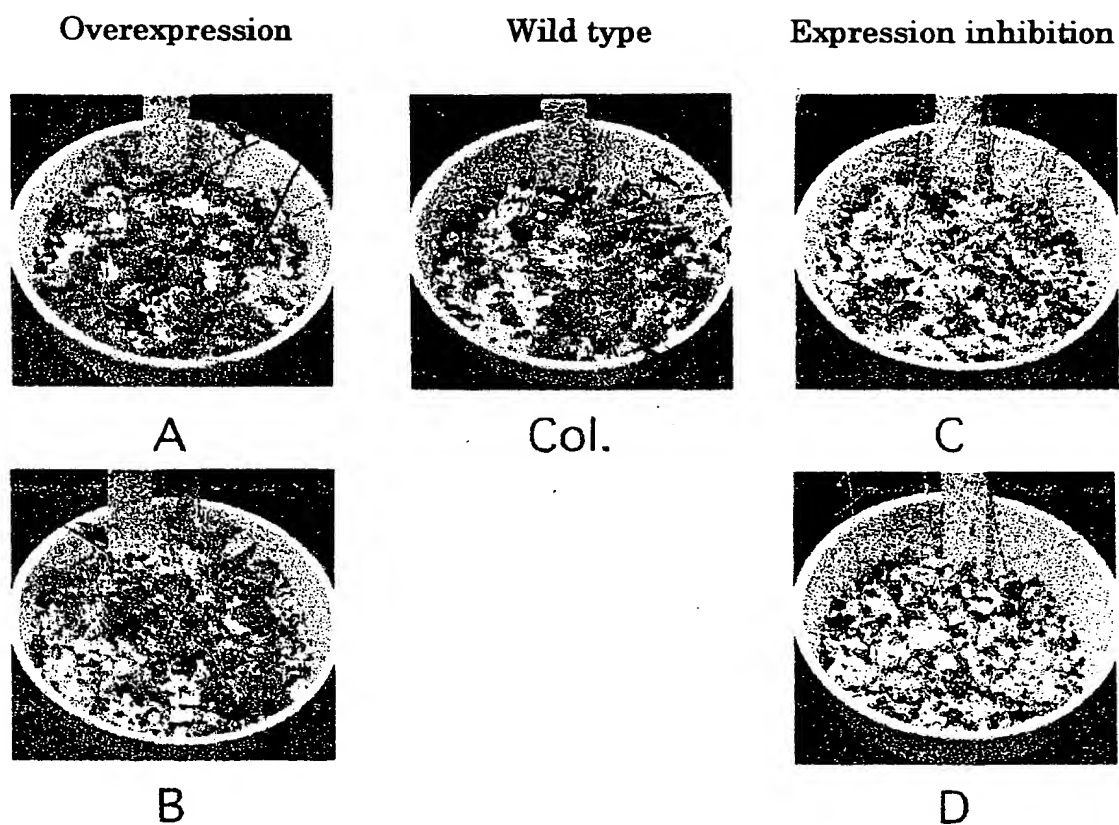


Figure 15



Water content of plants
14 days after tolerance evaluation

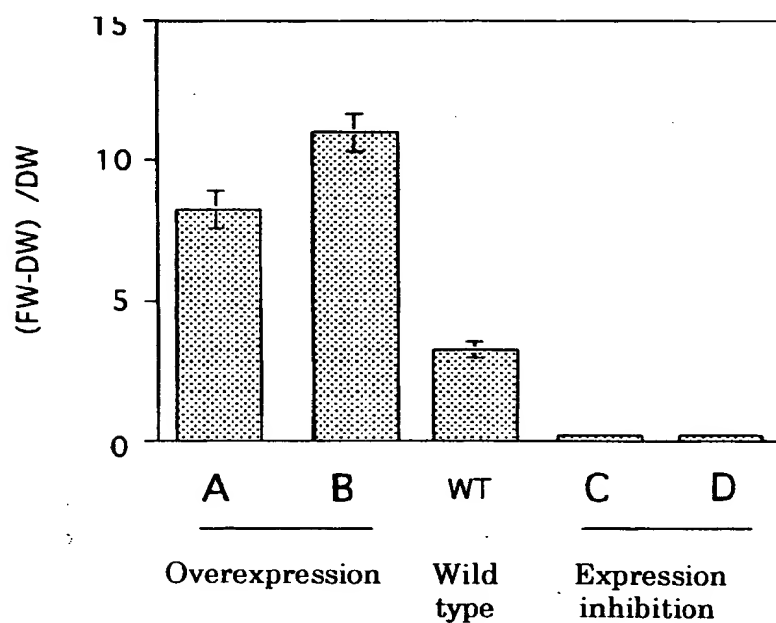
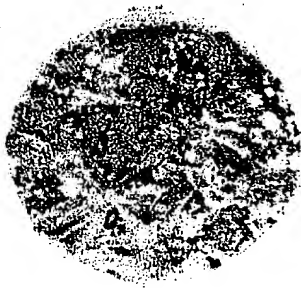


Figure 16

Overexpression

Wild type

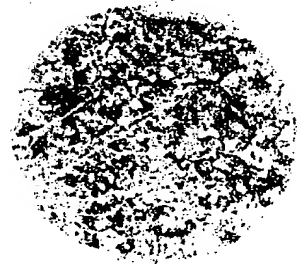
Expression
inhibition



A



Col.



C



B



D

6975825-01101